

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: McCarthy, Sean

(ii) TITLE OF INVENTION: NOVEL CRSP-1 COMPOSITIONS AND
THERAPEUTIC AND DIAGNOSTIC USES THEREFOR

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
- (B) STREET: One Post Office Square
- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02109-2170

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/842,898
- (B) FILING DATE: 17-APR-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Arnold, Beth E.
- (B) REGISTRATION NUMBER: 35,430
- (C) REFERENCE/DOCKET NUMBER: MAA-004.02

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-832-1000
- (B) TELEFAX: 617-832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 38..1087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG GGCAGCGGCT GCGGGCGCAG AGCGGAG ATG CAG CGG CTT GGG GCC Met Gln Arg Leu Gly Ala	55
1 5	
ACC CTG CTG TGC CTG CTG GCG GCG GCG GTC CCC ACG GCC CCC GCG Thr Leu Leu Cys Leu Leu Ala Ala Val Pro Thr Ala Pro Ala	103
10 15 20	
CCC GCT CCG ACG GCG ACC TCG GCT CCA GTC AAG CCC GGC CCG GCT CTC Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu	151
25 30 35	
AGC TAC CCG CAG GAG GAG GCC ACC CTC AAT GAG ATG TTC CGC GAG GTT Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val	199
40 45 50	
GAG GAA CTG ATG GAG GAC ACG CAG CAC AAA TTG CGC AGC GCG GTG GAA Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu	247
55 60 65 70	
GAG ATG GAG GCA GAA GAA GCT GCT GCT AAA GCA TCA TCA GAA GTG AAC Glu Met Glu Ala Glu Glu Ala Ala Lys Ala Ser Ser Glu Val Asn	295
75 80 85	
CTG GCA AAC TTA CCT CCC AGC TAT CAC AAT GAG ACC AAC ACA GAC ACG Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	343
90 95 100	
AAC GTT GGA AAT AAT ACC ATC CAT GTG CAC CGA GAA ATT CAC AAG ATA Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	391
105 110 115	
ACC AAC AAC CAG ACT GGA CAA ATG GTC TTT TCA GAG ACA GTT ATC ACA Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	439
120 125 130	
TCT GTG GGA GAC GAA GAA GGC AGA AGG AGC CAC GAG TGC ATC ATC GAC Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	487
135 140 145 150	
GAG GAC TGT GGG CCC AGC ATG TAC TGC CAG TTT GCC AGC TTC CAG TAC Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	535
155 160 165	
ACC TGC CAG CCA TGC CGG GGC CAG AGG ATG CTC TGC ACC CGG GAC AGT Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	583
170 175 180	
GAG TGC TGT GGA GAC CAG CTG TGT GTC TGG GGT CAC TGC ACC AAA ATG Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	631
185 190 195	
GCC ACC AGG GGC AGC AAT GGG ACC ATC TGT GAC AAC CAG AGG GAC TGC Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	679
200 205 210	
CAG CCG GGG CTG TGC TGT GCC TTC CAG AGA GGC CTG CTG TTC CCT GTG Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	727
215 220 225 230	

TGC ACA CCC CTG CCC GTG GAG GGC GAG CTT TGC CAT GAC CCC GCC AGC Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser 235 240 245	775
CGG CTT CTG GAC CTC ATC ACC TGG GAG CTA GAG CCT GAT GGA GCC TTG Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu 250 255 260	823
GAC CGA TGC CCT TGT GCC AGT GGC CTC CTC TGC CAG CCC CAC AGC CAC Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His 265 270 275	871
AGC CTG GTG TAT GTG TGC AAG CCG ACC TTC GTG GGG AGC CGT GAC CAA Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln 280 285 290	919
GAT GGG GAG ATC CTG CTG CCC AGA GAG GTC CCC GAT GAG TAT GAA GTT Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val 295 300 305 310	967
GGC AGC TTC ATG GAG GAG GTG CGC CAG GAG CTG GAG GAC CTG GAG AGG Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg 315 320 325	1015
AGC CTG ACT GAA GAG ATG GCG CTG AGG GAG CCT GCG GCT GCC GCT GCT Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala 330 335 340	1063
GCA CTG CTG GGA AGG GAA GAG ATT TAGATCTGGA CCAGGCTGTG GGTAGATGTG Ala Leu Leu Gly Arg Glu Glu Ile 345 350	1117
CAATAGAAAT AGCTAATTAA TTTCCCCANG TGTGTGCTTT AAGCGTGGGC TG	1169

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala 1 5 10 15
Val Pro Thr Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val 20 25 30
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn 35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys 50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95

 Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
 100 105 110

 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125

 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140

 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160

 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175

 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190

 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205

 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220

 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240

 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255

 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285

 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300

 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320

 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
 325 330 335

 Pro Ala Ala Ala Alà Ala Ala Leu Leu Gly Arg Glu Glu Ile
 340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCAGCGGC TTGGGGCCAC CCTGCTGTGC CTGCTGCTGG CGGC GGCGGT CCCCACGGCC 60
 CCCGCGCCCG CTCCGACGGC GACCTCGGCT CCAGTCAAGC CGGGCCCGGC TCTCAGCTAC 120
 CCGCAGGAGG AGGCCACCCCT CAATGAGATG TTCCGCGAGG TTGAGGAACG GATGGAGGAC 180
 ACGCAGCACA AATTGCGCAG CGCGGTGGAA GAGATGGAGG CAGAAGAACG TGCTGCTAAA 240
 GCATCATCAG AAGTGAACCT GGCAAACCTTA CCTCCCAGCT ATCACAATGA GACCAACACA 300
 GACACGAACG TTGGAAATAA TACCATCCAT GTGCACCGAG AAATTACAA GATAACCAAC 360
 AACCAAGACTG GACAAATGGT CTTTCAGAG ACAGTTATCA CATCTGTGGG AGACGAAGAA 420
 GGCAGAAGGA GCCACGAGTG CATCATCGAC GAGGACTGTG GGCCCAGCAT GTACTGCCAG 480
 TTTGCCAGCT TCCAGTACAC CTGCCAGCCA TGCCGGGGCC AGAGGATGCT CTGCACCCGG 540
 GACAGTGAGT GCTGTGGAGA CCAGCTGTGT GTCTGGGTC ACTGCACCAA AATGCCACC 600
 AGGGGCAGCA ATGGGACCAT CTGTGACAAC CAGAGGGACT GCCAGCCGGG GCTGTGCTGT 660
 GCCTTCCAGA GAGGCCTGCT GTTCCCTGTG TGACACACCC TGCCCGTGGA GGGCGAGCTT 720
 TGCCATGACC CCGCCAGCCG GCTTCTGGAC CTCATCACCT GGGAGCTAGA GCCTGATGGA 780
 GCCTTGGACC GATGCCCTTG TGCCAGTGGC CTCCCTGTGCC AGCCCCACAG CCACAGCCTG 840
 GTGTATGTGT GCAAGCCGAC CTTCTGGGG AGCCGTGACC AAGATGGGA GATCCTGCTG 900
 CCCAGAGAGG TCCCCGATGA GTATGAAGTT GGCAGCTTCA TGGAGGAGGT GCGCCAGGAG 960
 CTGGAGGACC TGGAGAGGAG CCTGACTGAA GAGATGGCGC TGAGGGAGCC TGCGGCTGCC 1020
 GCCGCTGCAC TGCTGGGAAG GGAAGAGATT 1050

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Arg	Gly	Glu	Gly	Pro	Ala	Pro	Arg	Arg	Arg	Trp	Leu	Leu	Leu
1															15

Leu	Ala	Val	Leu	Ala	Ala	Leu	Cys	Cys	Ala	Ala	Ala	Gly	Ser	Gly	Gly
															30
						20			25						

Arg Arg Arg Ala Ala Ser Leu Gly Glu Met Leu Arg Glu Val Glu Ala
 35 40 45

Leu Met Glu Asp Thr Gln His Lys Leu Arg Asn Ala Val Gln Glu Met
 50 55 60

Glu Ala Glu Glu Glu Gly Ala Lys Lys Leu Ser Glu Val Asn Phe Glu
 65 70 75 80

Asn Leu Pro Pro Thr Tyr His Asn Glu Ser Asn Thr Glu Thr Arg Ile
 85 90 95

Gly Asn Lys Thr Val Gln Thr His Gln Glu Ile Asp Lys Val Thr Asp
 100 105 110

Asn Arg Thr Gly Ser Thr Ile Phe Ser Glu Thr Ile Ile Thr Ser Ile
 115 120 125

Lys Gly Gly Glu Asn Lys Arg Asn His Glu Cys Ile Ile Asp Glu Asp
 130 135 140

Cys Glu Thr Gly Lys Tyr Cys Gln Phe Ser Thr Phe Glu Tyr Lys Cys
 145 150 155 160

Gln Pro Cys Lys Thr Gln His Thr His Cys Ser Arg Asp Val Glu Cys
 165 170 175

Cys Gly Asp Gln Leu Cys Val Trp Gly Glu Cys Arg Lys Ala Thr Ser
 180 185 190

Arg Gly Glu Asn Gly Thr Ile Cys Glu Asn Gln His Asp Cys Asn Pro
 195 200 205

Gly Thr Cys Cys Ala Phe Gln Lys Glu Leu Leu Phe Pro Val Cys Thr
 210 215 220

Pro Leu Pro Glu Glu Gly Glu Pro Cys His Asp Pro Ser Asn Arg Leu
 225 230 235 240

Leu Asn Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Val Leu Glu Arg
 245 250 255

Cys Pro Cys Ala Ser Gly Leu Ile Cys Gln Pro Gln Ser Ser His Ser
 260 265 270

Thr Thr Ser Val Cys Glu Leu Ser Ser Asn Glu Thr Arg Lys Asn Glu
 275 280 285

Lys Glu Asp Pro Leu Asn Met Asp Glu Met Pro Phe Ile Ser Leu Ile
 290 295 300

Pro Arg Asp Ile Leu Ser Asp Tyr Glu Glu Ser Ser Val Ile Gln Glu
 305 310 315 320

Val Arg Lys Glu Leu Glu Ser Leu Glu Asp Gln Ala Gly Val Lys Ser
 325 330 335

Glu His Asp Pro Ala His Asp Leu Phe Leu Gly Asp Glu Ile
 340 345 350